

# Documenting Discoveries of Diversity: How to Publish Novel Species

Microbrew Session by Jeff Newman, Lycoming College ([newman@lycoming.edu](mailto:newman@lycoming.edu))

NSF-funded project seeks to develop Standard Operating Procedures to discover and publish novel species.

a. Initial funding (MRI-R2 December 2009) supported purchase of Biolog Omnilog, MIDI Microbial Identification System for Fatty Acid Methyl Ester Analysis (FAME) and HPLC.

b. Additional funding being sought for technical support, bioinformatics support, **workshops**.

1. Read new guidelines to publish in the International Journal of Systematic and Evolutionary Microbiology (IJSEM).

Tindall B. J., Rossello-Mora R., Busse H.-J., Ludwig W. and Kämpfer P. (2010) Notes on the characterization of prokaryote strains for taxonomic purposes. IJSEM 60:249-266.

2. Compare your organisms's 16S rRNA sequence to TYPE strains at [www.EzTaxon.org](http://www.EzTaxon.org)

a. If less than 99% identical, use 4 more sequencing reactions to assemble (nearly) complete sequence of 27F-1492R PCR product using Contig Assemble Program CAP3 (google it)

b. Submit sequence **and traces** to Genbank.

c. Use ExTaxon Cart and SimTable functions to save related sequences for Multiple Sequence Alignment

3. Use MEGA4/MEGA5 (free) for Multiple Sequence Alignment, Distance Matrix Calculation and Construction of Neighbor Joining Tree (ARB/SILVA/RDP)

4. Obtain 3 or 4 most closely related type strains (and type species for genus) from Authors or Culture Collection (NRRL@ARS is free!) or check with Jeff Newman.

5. Research genus/family to identify specific guidelines/recommendations.

e.g. Bernardet, J. F., Nakagawa, Y. & Holmes, B. (2002). Proposed minimal standards for describing new taxa of the family Flavobacteriaceae and emended description of the family. Int J Syst Evol Microbiol 52, 1049–1070.

6. Repeat/conduct polyphasic characterization in parallel with related strains using standard techniques. We are developing expertise (Fall Sabbatical) to help with

a. Biolog GenIII plates (\$15 each – can visit or send strains)

b. MIDI/FAME (\$10 each - can visit or send strains)

c. GC composition analysis (\$ ?? each – can visit, send DNA)

d. Multi Locus Sequence Typing – ASM SURF student working this summer, we can send primers.

e. Cell wall amino acids/peptidoglycan type, polar lipids...???

Over next 3-5 years – genome sequencing cost will drop to <\$500, all published type strains will be available for comparison.

7. Send novel strain to 3-4 culture collections. Get Certificates

8. Write & Submit Paper!

**Collaborators sought for technical expertise, reviewing, type strains, workshops, grants.**